



ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/756,283A

DATE: 02/26/2002

TIME: 09:33:40

Input Set : A:\0623 1000000 seq list.txt

Output Set: N:\CRF3\02262002\I756283A.raw

5 <110> APPLICANT: Chernajovsky, Yuti
 6 Dreja, Hanna Stina
 7 Adams, Gillian
 10 <120> TITLE OF INVENTION: Latent Fusion Protein
 13 <130> FILE REFERENCE: 0623.1000000
 16 <140> CURRENT APPLICATION NUMBER: US 09/756,283A
 18 <141> CURRENT FILING DATE: 2001-01-09
 21 <160> NUMBER OF SEQ ID NOS: 100
 24 <170> SOFTWARE: PatentIn version 3.0
 28 <210> SEQ ID NO: 1
 30 <211> LENGTH: 15
 32 <212> TYPE: PRT
 C--> 34 <213> ORGANISM: Artificial
 38 <220> FEATURE:
 40 <223> OTHER INFORMATION: MMP cleavage site including linker sequence
 42 <400> SEQUENCE: 1
 44 Gly Gly Gly Gly Ser Pro Leu Gly Leu Trp Ala Gly Gly Gly Ser
 45 1 5 10 15
 47 <210> SEQ ID NO: 2
 49 <211> LENGTH: 52
 51 <212> TYPE: DNA
 C--> 53 <213> ORGANISM: Artificial
 57 <220> FEATURE:
 59 <223> OTHER INFORMATION: Sense oligo
 61 <400> SEQUENCE: 2
 62 aattcggggg aggcggatcc ccgctcgggc tttgggcggg agggggctca gc 52
 65 <210> SEQ ID NO: 3
 67 <211> LENGTH: 52
 69 <212> TYPE: DNA
 C--> 71 <213> ORGANISM: Artificial
 75 <220> FEATURE:
 77 <223> OTHER INFORMATION: Antisense oligo
 79 <400> SEQUENCE: 3
 80 ggccgctgag cccctcccg cccaaagccc gagcggggat ccgcctcccc cg 52
 83 <210> SEQ ID NO: 4
 85 <211> LENGTH: 29
 87 <212> TYPE: DNA
 C--> 89 <213> ORGANISM: Artificial
 93 <220> FEATURE:
 95 <223> OTHER INFORMATION: Sense Primer
 97 <400> SEQUENCE: 4
 98 ccaagcttat gccgccctcc gggctgcgg 29
 101 <210> SEQ ID NO: 5

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103 <211> LENGTH: 29
105 <212> TYPE: DNA
C--> 107 <213> ORGANISM: Artificial
111 <220> FEATURE:
113 <223> OTHER INFORMATION: Antisense Primer
115 <400> SEQUENCE: 5
116 ccgaattcgc ttgcagatg ctgggccct 29
119 <210> SEQ ID NO: 6
121 <211> LENGTH: 31
123 <212> TYPE: DNA
C--> 125 <213> ORGANISM: Artificial
129 <220> FEATURE:
131 <223> OTHER INFORMATION: Sense Primer
133 <400> SEQUENCE: 6
134 cgcggccgca atcaactata agcagctcca g 31
137 <210> SEQ ID NO: 7
139 <211> LENGTH: 32
141 <212> TYPE: DNA
C--> 143 <213> ORGANISM: Artificial
147 <220> FEATURE:
149 <223> OTHER INFORMATION: Antisense Primer
151 <400> SEQUENCE: 7
152 ggtctagatc agttttggaa gtttctggta ag 32
155 <210> SEQ ID NO: 8
157 <211> LENGTH: 29
159 <212> TYPE: DNA
C--> 161 <213> ORGANISM: Artificial
165 <220> FEATURE:
167 <223> OTHER INFORMATION: Sense Primer
169 <400> SEQUENCE: 8
170 ccaagcttat gaacaacagg tggatcctc 29
173 <210> SEQ ID NO: 9
175 <211> LENGTH: 29
177 <212> TYPE: DNA
C--> 179 <213> ORGANISM: Artificial
183 <220> FEATURE:
185 <223> OTHER INFORMATION: Antisense Primer
187 <400> SEQUENCE: 9
188 ccgaattcgt ttggaagtt tctggttaag 29
191 <210> SEQ ID NO: 10
193 <211> LENGTH: 31
195 <212> TYPE: DNA
C--> 197 <213> ORGANISM: Artificial
201 <220> FEATURE:
203 <223> OTHER INFORMATION: Sense Primer
205 <400> SEQUENCE: 10
206 cgcggccgca ctatccacct gcaagactat c 31
209 <210> SEQ ID NO: 11
211 <211> LENGTH: 32

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213 <212> TYPE: DNA
C--> 215 <213> ORGANISM: Artificial
219 <220> FEATURE:
221 <223> OTHER INFORMATION: Antisense Primer
223 <400> SEQUENCE: 11
224 ggtctagatc agctttgcag atgctgggcc ct 32
227 <210> SEQ ID NO: 12
229 <211> LENGTH: 23
231 <212> TYPE: DNA
C--> 233 <213> ORGANISM: Artificial
237 <220> FEATURE:
239 <223> OTHER INFORMATION: Sense Primer
241 <400> SEQUENCE: 12
242 cgcccatggc gccttcgggg cct 23
245 <210> SEQ ID NO: 13
247 <211> LENGTH: 29
249 <212> TYPE: DNA
C--> 251 <213> ORGANISM: Artificial
255 <220> FEATURE:
257 <223> OTHER INFORMATION: Antisense Primer
259 <400> SEQUENCE: 13
260 ccgaattcgc tgtgcagggtg ctgggccct 29
263 <210> SEQ ID NO: 14
265 <211> LENGTH: 5
267 <212> TYPE: PRT
C--> 269 <213> ORGANISM: Artificial
273 <220> FEATURE:
275 <223> OTHER INFORMATION: Flexible linker
277 <400> SEQUENCE: 14
279 Gly Gly Gly Gly Ser
280 1 5
282 <210> SEQ ID NO: 15
284 <211> LENGTH: 6
286 <212> TYPE: PRT
C--> 288 <213> ORGANISM: Artificial
292 <220> FEATURE:
294 <223> OTHER INFORMATION: Cleavage site
296 <400> SEQUENCE: 15
298 Pro Leu Gly Leu Trp Ala
299 1 5
301 <210> SEQ ID NO: 16
303 <211> LENGTH: 8
305 <212> TYPE: PRT
C--> 307 <213> ORGANISM: Artificial
311 <220> FEATURE:
313 <223> OTHER INFORMATION: Flexible portion
315 <400> SEQUENCE: 16
317 Gly Gly Gly Gly Ser Ala Ala Ala
318 1 5

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320 <210> SEQ ID NO: 17
322 <211> LENGTH: 4
324 <212> TYPE: PRT
C--> 326 <213> ORGANISM: Artificial
330 <220> FEATURE:
332 <223> OTHER INFORMATION: Core of cleavage site
334 <400> SEQUENCE: 17
336 Pro Leu Gly Leu
337 1
339 <210> SEQ ID NO: 18
341 <211> LENGTH: 4
343 <212> TYPE: PRT
C--> 345 <213> ORGANISM: Artificial
349 <220> FEATURE:
351 <223> OTHER INFORMATION: Core of cleavage site
353 <400> SEQUENCE: 18
355 Pro Leu Gly Ile
356 1
358 <210> SEQ ID NO: 19
360 <211> LENGTH: 1376
362 <212> TYPE: DNA
C--> 364 <213> ORGANISM: Artificial
368 <220> FEATURE:
370 <223> OTHER INFORMATION: LAP-mIFNbeta construct
372 <220> FEATURE:
374 <221> NAME/KEY: CDS
376 <222> LOCATION: (1)..(1368)
380 <400> SEQUENCE: 19
381 atg ccg ccc tcc ggg ctg cgg ctg ctg ccg ctg ctg cta ccg ctg ctg      48
382 Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
383 1 5 10 15
385 tgg cta ctg gtg ctg acg cct ggc ccg ccg gcc gcg gga cta tcc acc      96
386 Trp Leu Leu Val Leu Thr Pro Gly Pro Pro Ala Ala Gly Leu Ser Thr
387 20 25 30
389 tgc aag act atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc      144
390 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
391 35 40 45
393 atc cgc ggc cag atc ctg tcc aag ctg cgg ctc gcc agc ccc ccg agc      192
394 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
395 50 55 60
397 cag ggg gag gtg ccg ccc ggc ccg ctg ccc gag gcc gtg ctc gcc ctg      240
398 Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
399 65 70 75 80
401 tac aac agc acc cgc gac cgg gtg gcc ggg gag agt gca gaa ccg gag      288
402 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu
403 85 90 95
405 ccc gag cct gag gcc gac tac tac gcc aag gag gtc acc cgc gtg cta      336
406 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
407 100 105 110

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409 atg gtg gaa acc cac aac gaa atc tat gac aag ttc aag cag agt aca      384
410 Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
411      115      120      125
413 cac agc ata tat atg ttc ttc aac aca tca gag ctc cga gaa gcg gta      432
414 His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
415      130      135      140
417 cct gaa ccc gtg ttg ctc tcc cgg gca gag ctg cgt ctg ctg agg agg      480
418 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Arg
419 145      150      155      160
421 ctc aag tta aaa gtg gag cag cac gtg gag ctg tac cag aaa tac agc      528
422 Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser
423      165      170      175
425 aac aat tcc tgg cga tac ctc agc aac cgg ctg ctg gca ccc agc gac      576
426 Asn Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp
427      180      185      190
429 tcg cca gag tgg tta tct ttt gat gtc acc gga gtt gtg cgg cag tgg      624
430 Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp
431      195      200      205
433 ttg agc cgt gga ggg gaa att gag ggc ttt cgc ctt agc gcc cac tgc      672
434 Leu Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys
435      210      215      220
437 tcc tgt gac agc agg gat aac aca ctg caa gtg gac atc aac ggg ttc      720
438 Ser Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe
439 225      230      235      240
441 act acc ggc cgc cga ggt gac ctg gcc acc att cat ggc atg aac cgg      768
442 Thr Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg
443      245      250      255
445 cct ttc ctg ctt ctc atg gcc acc ccg ctg gag agg gcc cag cat ctg      816
446 Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu
447      260      265      270
449 caa agc gaa ttc ggg gga ggc gga tcc ccg ctc ggg ctt tgg gcg gga      864
450 Gln Ser Glu Phe Gly Gly Gly Gly Ser Pro Leu Gly Leu Trp Ala Gly
451      275      280      285
453 ggg ggc tca gcg gcc gca atc aac tat aag cag ctc cag ctc caa gaa      912
454 Gly Gly Ser Ala Ala Ala Ile Asn Tyr Lys Gln Leu Gln Leu Gln Glu
455      290      295      300
457 agg acg aac att cgg aaa tgt cag gag ctc ctg gag cag ctg aat gga      960
458 Arg Thr Asn Ile Arg Lys Cys Gln Glu Leu Leu Glu Gln Leu Asn Gly
459 305      310      315      320
461 aag atc aac ctc acc tac agg gcg gac ttc aag atc cct atg gag atg      1008
462 Lys Ile Asn Leu Thr Tyr Arg Ala Asp Phe Lys Ile Pro Met Glu Met
463      325      330      335
465 acg gag aag atg cag aag agt tac act gcc ttt gcc atc caa gag atg      1056
466 Thr Glu Lys Met Gln Lys Ser Tyr Thr Ala Phe Ala Ile Gln Glu Met
467      340      345      350
469 ctc cag aat gtc ttt ctt gtc ttc aga aac aat ttc tcc agc act ggg      1104
470 Leu Gln Asn Val Phe Leu Val Phe Arg Asn Asn Phe Ser Ser Thr Gly
471      355      360      365
473 tgg aat gag act att gtt gta cgt ctc ctg gat gaa ctc cac cag cag      1152

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/756,283A

DATE: 02/26/2002

TIME: 09:33:42

Input Set : A:\0623 1000000 seq list.txt

Output Set: N:\CRF3\02262002\I756283A.raw

L:34 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:53 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:71 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:89 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:125 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:143 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:161 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:179 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:197 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:233 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:251 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:269 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:288 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:307 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:326 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:345 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:364 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:504 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:637 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:775 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55